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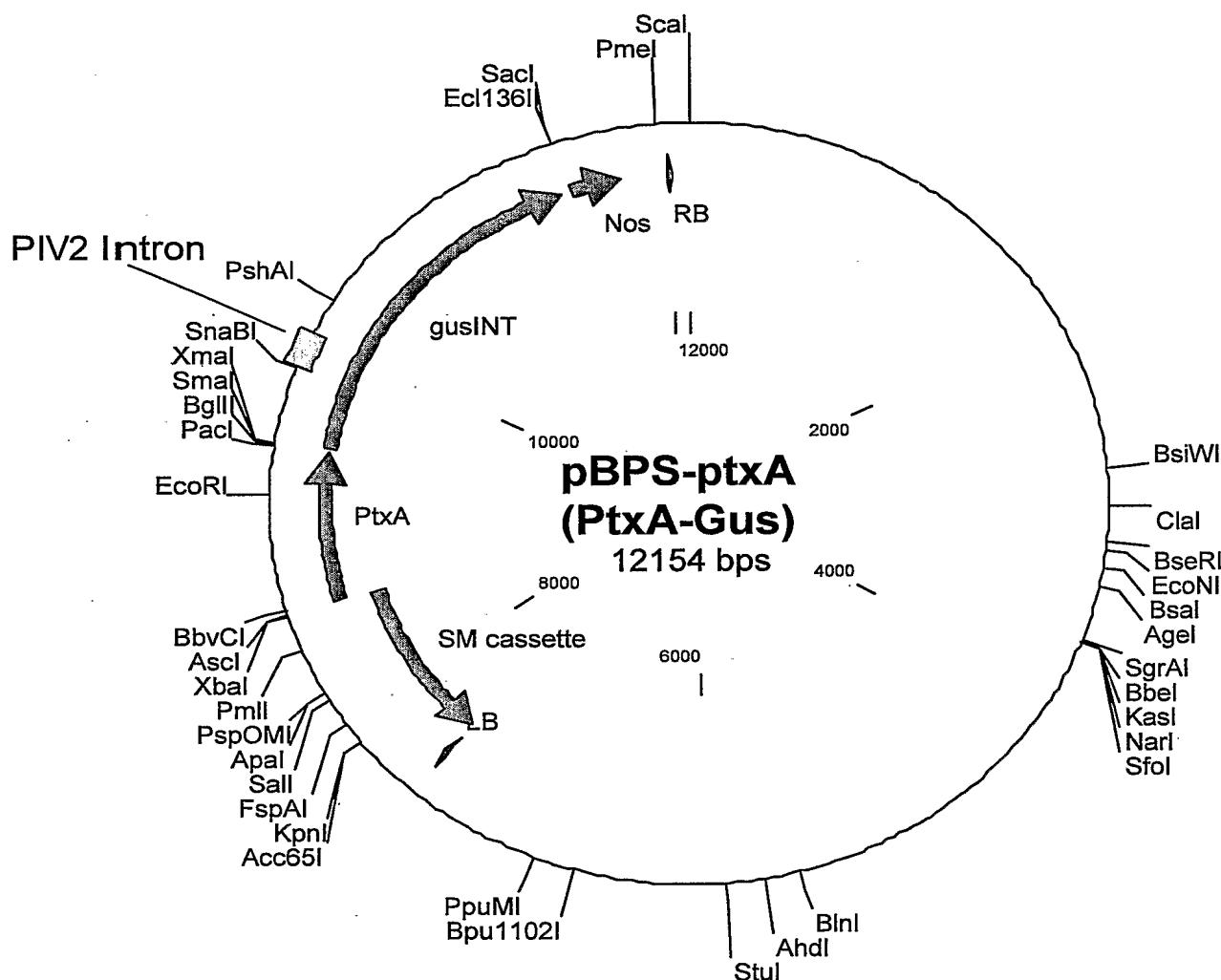


Fig. 1

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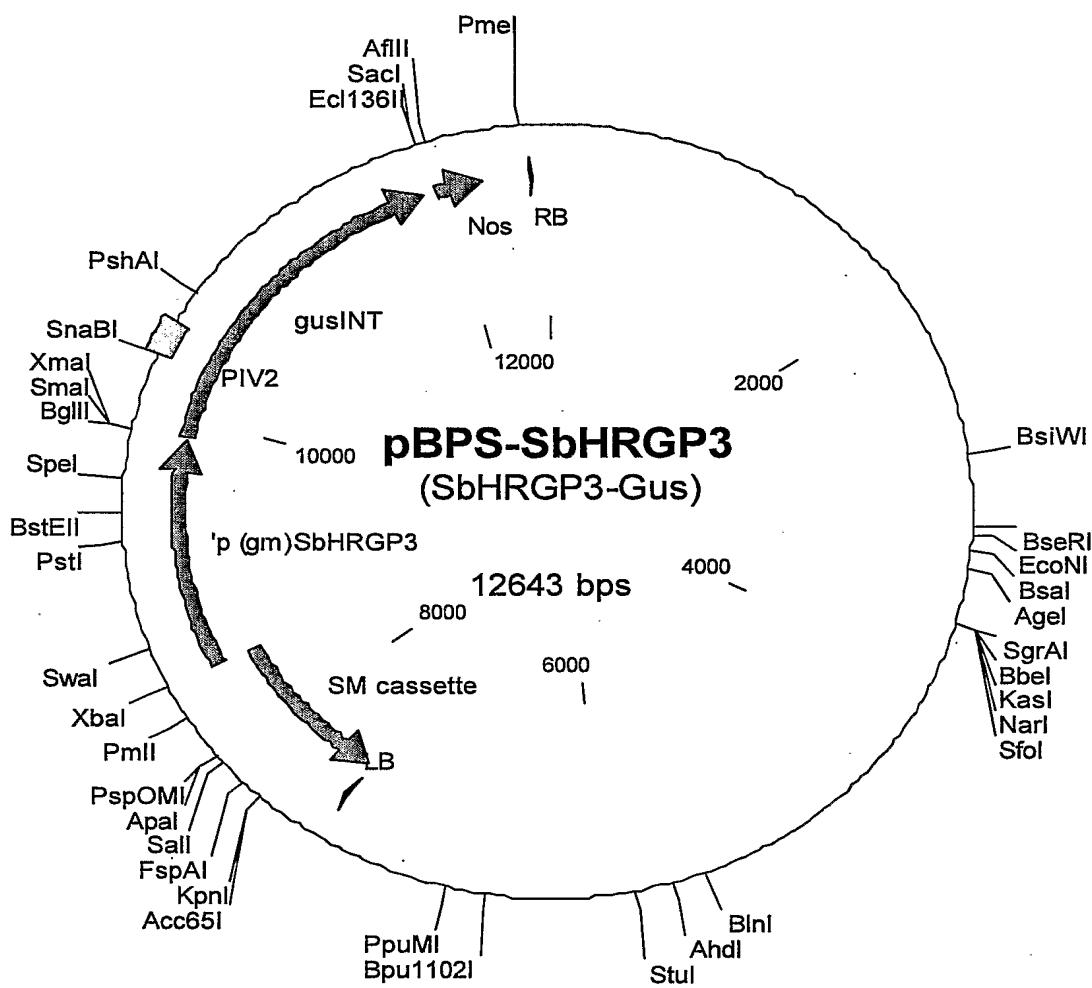


Fig. 2

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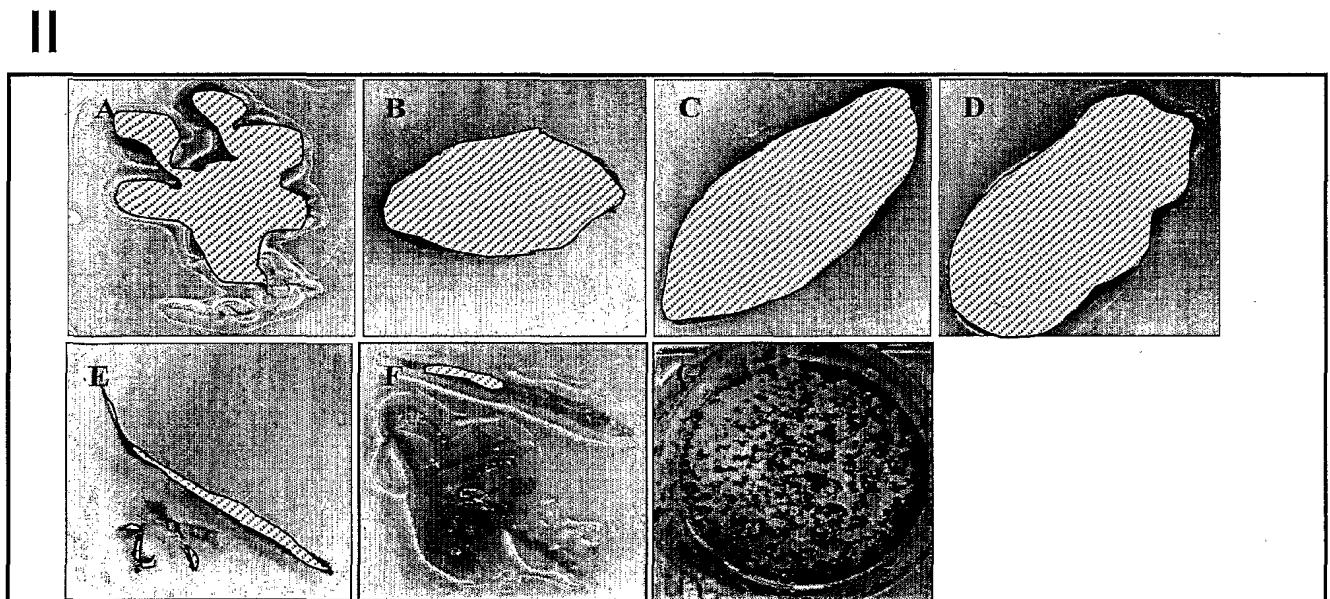
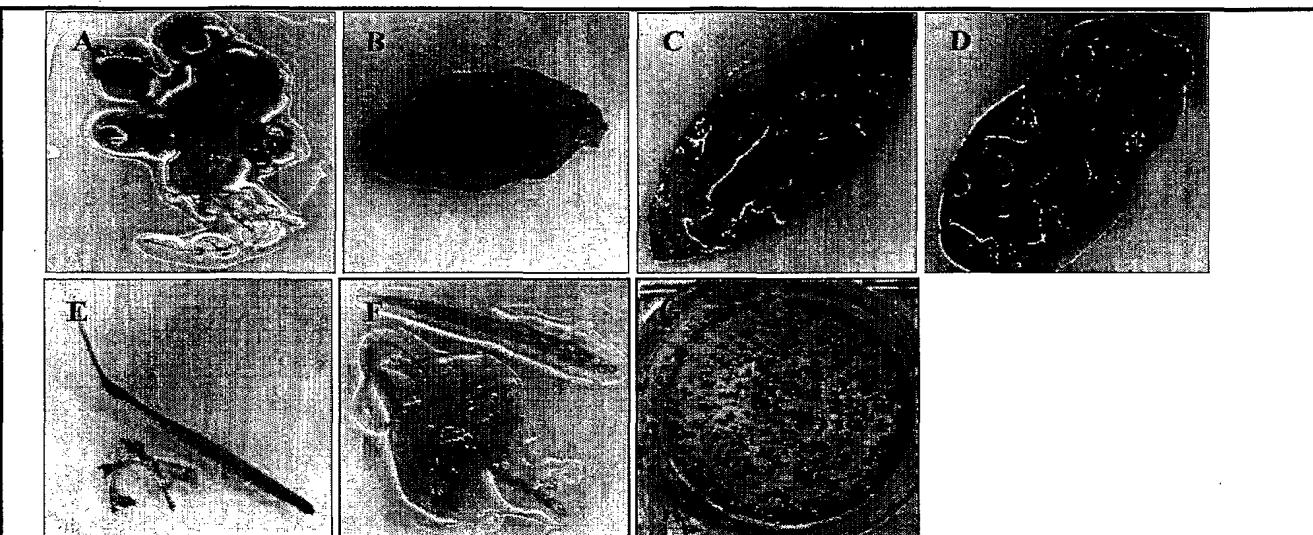


Fig 3

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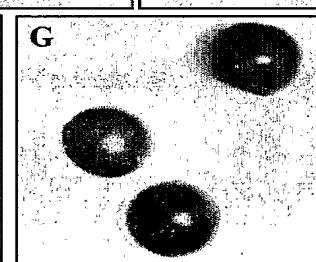
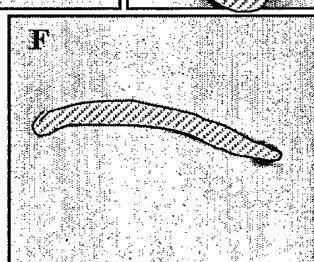
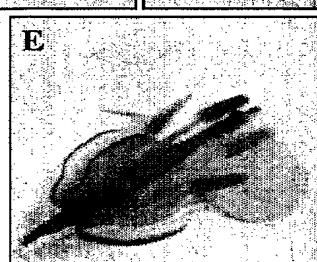
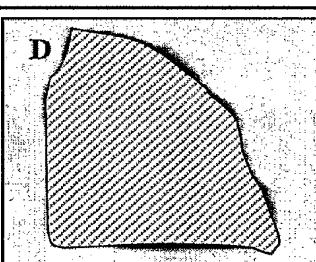
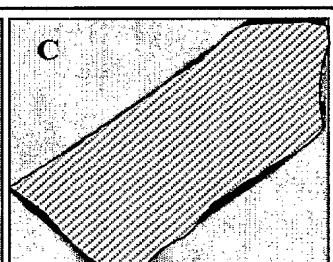
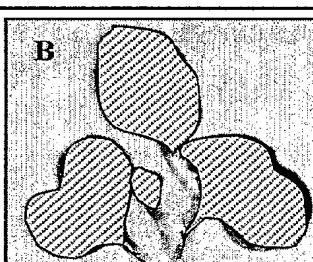
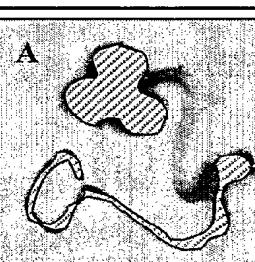
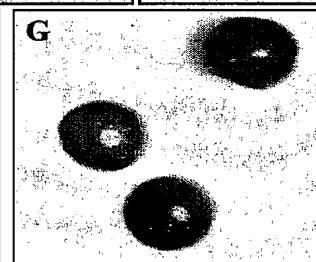
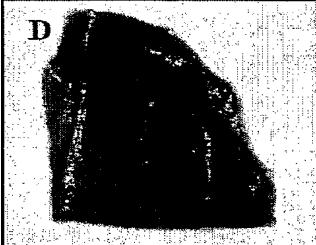
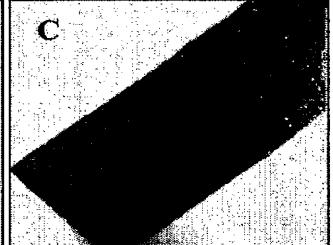
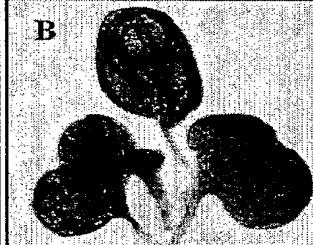
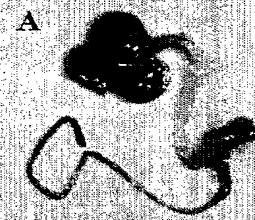


Fig 4

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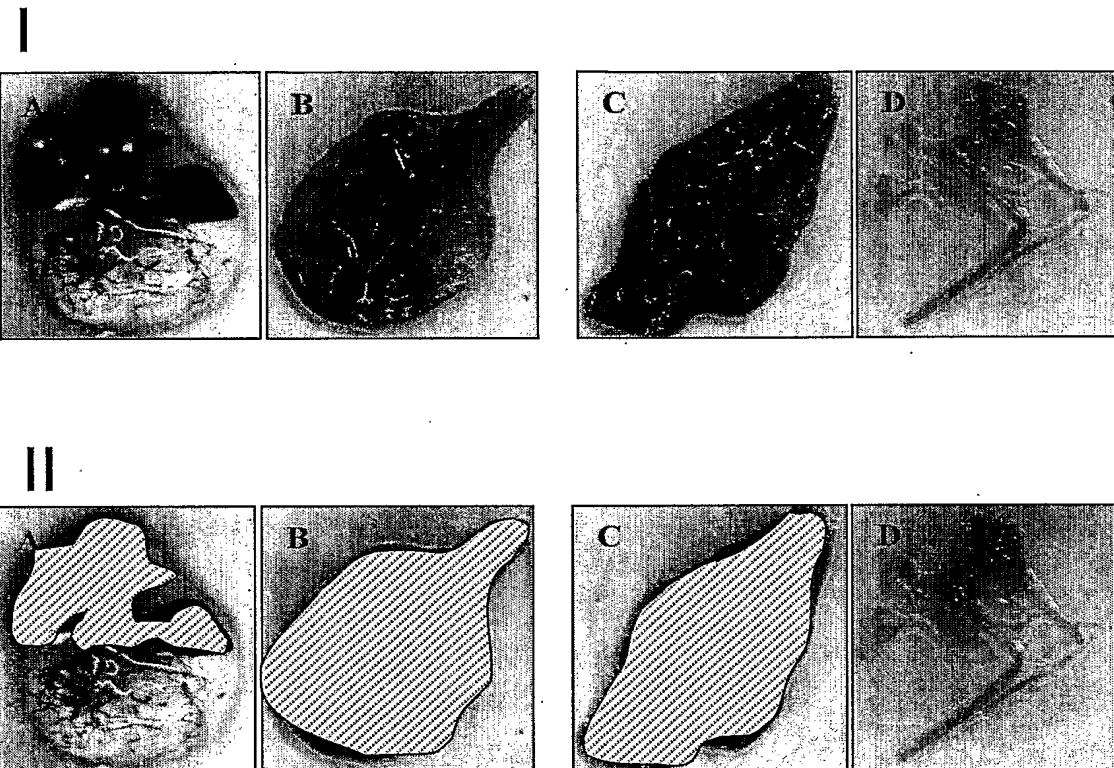


Fig 5

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	1	50
A	(1) MANFAIANVLILLLNLSTLLNVACPYCPYPSPKPKPTHKPPIVKPPVHK-	
B	(1) MANYALANVFILLLNLSLLIVLACPYCPYPSPKPKPTHHPPIVKPPVHKR	
C	(1) -----	
D	(1) -PHVKPPSTPKHPKDPPHVVKPPSTPKQPPYVKPPTPKHPPHVKKPS---	
E	(1) MGKHGLATWLVILLNFATLLTSACSYCPSPSPP-----	
F	(1) MGSRVLASFFVFLIFTVITLPPTIQACTPCTRPHPPVPKP-----	
Consensus	(1) MA ALAS ILLN STLL LAC YCPYPSP PP PP VKPP	
	51	100
A	(50) -----PPKPQPCPPPSSSPKPPHVKPPPHPKPPAVHP	
B	(51) RKYSPTPKPPVHKPPRYPPKSPCPCPPSSTPKPPHVKPPPHPKPPVHP	
C	(1) -----RAESART	
D	(47) -----TPKHPKHPP-----QKPCPPPSHHGPKPPIVKP	
E	(35) -----KPP-----KVKHPLPLPPKHPHVKP	
F	(41) -----PQHGGGGGGSKPPPHGGKGKGKPP	
Consensus	(51) PK PP K PH PPP H PKPP VKP	
	101	150
A	(83) PHVPKPP-AVHPPHVKPPVVHPIVHPPYVPK-----PPVVKPP-----	
B	(101) PHVPKP--PVHPPYVPKPIVKPIVHPPYVPK-----PPVVKPPPYVPK	
C	(8) HHMFQP---HPP-YVPKPIVKPIVHPPYVPK-----PPVVKPP-----	
D	(75) PHVPRPP-IVHPPPIVSPPSTPKPPKTPFPTKPPSIPPIVSPP-----	
E	(57) PHTPMPM-----PNPPAVKPPYVPK-----PPVVEPP-----	
F	(67) PHGGKGGGGPPHHGGGGGGKSPPVVRPPPVVVRP---PPIIRPP-----	
Consensus	(101) PHVPKP VHPPYVPKPIV PPIVHPPYVPK PPVVKPP	
	151	200
A	(122) --VVKPPHVPKPPVVPTPPYIPKPPIVFPFHVKPLPP--VVPVTPPYVPK	
B	(144) PPVVRPPYVPKPPVVPTPPYVPKPPVVRPPYVPKPP--VVPVTPPYVPK	
C	(44) -----PYVPKPPVVRPPYVPKPP--VVPVTPPYVLS	
D	(119) -----IVYPPITPTPPIVHPPVTPKPPSPTPPIVSPPIVY	
E	(83) -----YVPKPPVVKPPYVPKPP--PVVEPPYMP	
F	(109) -----PVVYPPPIVRPPPITRPPIIIQPPPVTT	
Consensus	(151) V PPYVPKPIVRRPPYVPKPP VVPVTPPYVLS	
	201	250
A	(168) P----PIVFPPHVPLPPVVPTPPYVP-----KPIVFPFHVKPLPPVVP	
B	(192) PPIVKPPIVFPPHVPLPPVVPSPPYVPSPIVKPPIVFPFHVKPLPPVVP	
C	(73) HHCFP-TTVSTSSCTITTLCTNTPIVN-----HQLFFHHMFFYLPVVP	
D	(154) PPITPTPPVVSPIIPTPPIVSPPFVPN-----PPVVP	
E	(108) -----	
F	(140) PPGLLPPITTGG--LLPPVTTGGLLP-----PVTTGG	
Consensus	(201) PP PIV PP V L P V SPPPIVP I F PL PVVP	
	251	300
A	(208) VTPPYVPLPPVVPTPPFVPTPPIITPPTPTVVPVSPSETCPFFFFPTV	
B	(242) VTPPYVQPP---PIVTPPTPTPPIVTPPVVSPPTP--PSETPCPPPLVP	
C	(116) VTPPYVQPT-----TYCNSTNTNTSNWTPPTP--PSETLVLPPPLVP	
D	(186) IPPPYVPSP-----PVVTPPIVPTPPTPCPP-----PPPPAI	
E	(108) -----H	
F	(173) LLPIIINPP-----PVTVPPPSSGYPPYG-----PPSGG	
Consensus	(251) VTPPYVQPP P IV PP TPPTP PSET PPPP	

Fig. 6a

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	301	350
A	(258) VPYPPPAQPTCSIDALKGACVDVLGGLIHIGIGGSAKQTCCPLLQGLVD	
B	(287) YPPTPPAQQTCSIDALKGACVDVLGGLIHIGIGGSAKQTCCPLLQGLVD	
C	(156) YP-PPPAQQTCSIDALKGACVDVLGGLIHIGIGGSAKQTCCPLLQGLVD	
D	(219) IP-SPPAQPTCPIDALKGACVDVLGGLIHIGIGGSAKQTCCPLLGGLVD	
E	(109) DT-----L---KLGACVDLLGGLVHIGIGGSSAKDTCCPVLQGLVD	
F	(202) GGGGGGKQPTCPINALKGACVDVLGGLIHIGLGNPVENVCCPVLQGLLE	
Consensus	(301) P PPAQPTCSIDALKGACVDVLGGLIHIGIGGSAKQTCCPLLQGLVD	
		351
A	(308) LDAAVCLCTTIRLKLLNINLVIPLALQVLID-CGKTPPEGFKCPSS-	
B	(337) LDAAICLCTTIRLKLLNINLVIPLALQVLID-CGKTPPEGFKCPAY-	
C	(205) LDAAICLCTTIRLKLLNINLVIPLALQVLID-CGKTPPEGFKCPAS-	
D	(268) LDAAICLCTTIRLKLLNINIILPIALQVLIDDCGKYPPKDFKCPST-	
E	(146) LDAAVCLCTAIKVVKLLNVNIIIPIALQVLVG-CGKTPPSGFQCPA--	
F	(252) LEAAVCLCTTIRLKLLNINIFIPLALQALIT-CGINPPSGFVCPLT	
Consensus	(351) LDAAICLCTTIRLKLLNINIVIPLALQVLID CGKTPPEGFKCPAS	

Fig. 6b

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	551	600
B	(551) AAAAACTAAAAATAATTCTCCTGATTATATGAAATGACATTTTT	
A	(1) -----CGCAATTTTT	
Consensus	(551) G ATTTTT	
	601	650
B	(601) TGGAACATGAAGG-GTATTGATTTACCACCTTACACCT--TTCAAA	
A	(12) GTGAAGCTGAGGGAGGATTGGATTTACACCTATTCAAAAGTCATTCAAA	
Consensus	(601) GAA TGA GG G ATTG TTTAC C TT A A T TTCAAA	
	651	700
B	(648) G-----CCATTCAAGGATGAATATAGATTTGGCGATCAAACAC	
A	(62) GTTGTCCCTCCATTCAAGGATGAATGTAGATTTCAAGCATCAAACAC	
Consensus	(651) G CCATTCAAGGATGAAT TAGATTTT ATCAAACAC	
	701	750
B	(689) AAGAATCATTACGATAACATGCTTGGAACACACACATGCTAAATTAAT	
A	(112) AAGAATCACTAGCATAACATGCTTGGAACACACACACACACACAC	
Consensus	(701) AAGAATCA TA ATAACATGCTTG AAC CACACA CTTAAATTAAT	
	751	800
B	(739) GGTGGAGTATCAAAT---TTTAAAT-ATTGTTGTCAAT-ACATACCC	
A	(160) GTAGGAATATCAAATCCAATATAAAATCATAGTTGTCAATTACATACTC	
Consensus	(751) G T GGA TATCAAAT T TAAAAT AT GTTGTCAAT ACATAC C	
	801	850
B	(783) CGTCAATCTTCTTTTACCCAATAAACATTGAAATGTTGCTTCTTC	
A	(210) AATCAAGTCCCTTCTTACCCAATAAACATCAACATATTGCTTCTTC	
Consensus	(801) TCAA CTTT TTTACCCAATAAACAT A AT TTGCTTCTT C	
	851	900
B	(833) GTTAAGCATAAAAACATCAAAGTCTA-----GCAAAATGTTGTTTGC	
A	(260) ATTAAGCATAAAACATCAAAGTCTAAAGACTAGCAAAATGTTGTTTGTAG	
Consensus	(851) TTAAGCATA AAACATCAAAGTCTA GCAAAATGTTGTTTGTAG	
	901	950
B	(877) GATGACACATTCATA--TAGTTAAAGGATGCATGATTGATTACAAA	
A	(310) GATGACACATTCATACATAGTTAAAAGATACTTGATTGATTACAAA	
Consensus	(901) GATGACACATTCATA TAGTTAAA GAT C TGATTGATTACAAA	
	951	1000
B	(925) ACAAAATACTAATAATTCTAGCACAAAGTTAAAGCAAGATTATAAAGCT	
A	(360) AGAAATTACCAATAGTT-TAGCACAAAGTCTAAAGCATAATTA--AAGCA	
Consensus	(951) A AAA TAC AATA TT TAGCACAAAGT TAAAGCA ATTA AAGC	
	1001	1050
B	(975) TCATAGCATGTGGATATTCAATTAGAAATATAGATTA-GATTGCCCTT	
A	(407) TCA---CATGTGCAGATTAT---GAAAAAAAGATTAAGATTGCCCTT	
Consensus	(1001) TCA CATGTG A ATT AT GAAA A AGATTA GATTGCCCTT	
	1051	1100
B	(1024) CATCACGGGTC---TAACAGCACCCTGTCACTACATGTCAAAAAA--TG	
A	(451) CATCACGGGTCGAATAATAGCACTACTGTCACTACATGTAAAAAAATG	
Consensus	(1051) CATCACGGGTC TAA AGCAC ACTGTCACTACATGT AAAAAA TG	
	1101	1150
B	(1069) TCCTCTAGTACAGCACCGCTTTACTTGATTCCCTTGTCCATGCATGA	
A	(501) TCCTCTAGTACATCAAACCTTTCCATTGATTCCCTTATCC---ATGA	
Consensus	(1101) TCCTCTAGTAC A CA TTTT TTGATTCCCTT TCC ATGA	
	1151	1200
B	(1119) AAAAAATCAAAACAATATTGGACACACAAACTTGCCCCCACTTCCTT	
A	(547) AAAAAATAAACAAATTCTTAAGACACACAAAAAAATGGCCCCACAT-CCTTT	
Consensus	(1151) AAAAAAT AA A A T TT GACACA AAA TG CCCCAC T CCTTT	

Fig. 7a

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	1201	1250
B	(1169) TTCTTTCTGCCCTAGTTGTTGAGACTCATATTGATCAAATTGGCTAT	
A	(596) ---TTTCTGGCCTAGTTGTTGA-----	
Consensus	(1201) TTTCTG CCTAGTTGTTGA	
	1251	1300
B	(1219) GAATTCAAACAAAAATTCACTCTACCCATTGCATGTGT---GGGGCCCA	
A	(617) -----A---TTCATTCTAACTCTGAATATGTAACGAGGCCCA	
Consensus	(1251) A TTCA TCTA C TTG AT TGT G GGCCC	
	1301	1350
B	(1266) CATATAAATCCATGAAGGATTCAATGTCCATCCAAGTCAATGATTCAAC	
A	(652) C-TAAAAATCAAT-----CAATGATTTAAC	
Consensus	(1301) C TA AAATC AT CAATGATT AAC	
	1351	1400
B	(1316) ATATATAACATTGAATAATTAAATTCCAATTGCAGTATTATGATTTAGA	
A	(676) ATAAAAAAA---TGAATAGTTAATTCCAATTGC-----	
Consensus	(1351) ATA A AA TGAATA TTTAATTCCAATTGC	
	1401	1450
B	(1366) TTGATTGCTGCAAATACGGTCCGTGAATGTGATCACTCACGAGAAAGAGGT	
A	(707) -----TGCAACATGGTCCGTGAATATGA---CTCACGAGAAAGATAT	
Consensus	(1401) TGCAA A GGTCCGTGAAT TGA CTCACGAGAAAGA T	
	1451	1500
B	(1416) ATCAAAATTCAAGGTATTTATTATTAAACAAATAAAATTCAAGG	
A	(746) ATCAAAATATCAA-----AATTCATAG	
Consensus	(1451) ATCAAAAT TCAA AATTTCA G	
	1501	1550
B	(1466) TCTTGTTCACCATAAACCTCCTCACTCACACCCAATTCTCTTAAGTGT	
A	(769) TTTTTTCACCATAAACCTCATCACTCATTC--TATTTTTTAAGTGC	
Consensus	(1501) T TT TTCACCATAAACCTC TCACCTCA C ATT T TTAAGTG	
	1551	1600
B	(1516) ATGACTTCATAGTAC--ACTACACTACTTCTTGAAACATGGCTAACTA	
A	(817) AAAGCTTCATAGTAGTGAGCACACACATTACACTAAAATCTCGAAACTT	
Consensus	(1551) A CTTCATAGTA A ACAC TT C T AAA T AACT	
	1601	1650
B	(1564) TGCTCTAGCCAATGTTCATCCTCTTGAACCTGAGTACCTTACTCA	
A	(867) A-----	
Consensus	(1601)	

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	1	50
SEQ ID NO: 9	(1)	---
SEQ ID NO: 8	(1)	AAGCTTTCAACAATCATGCCCATGTCAAGTGTAAAACAGGTTACCTCT
SEQ ID NO: 7	(1)	AAGCTTTCAACAATCATGCCCATGTCAAGTGTAAAACAGGTTACCTCT
Consensus	(1)	AAGCTTTCAACAATCATGCCCATGTCAAGTGTAAAACAGGTTACCTCT
		51
SEQ ID NO: 9	(48)	CTTAAATAACCGTATTAAAATGCTGAATGATGTATATATGTGGGTTCAAA
SEQ ID NO: 8	(51)	CTTAAATAACCGTATTAAAATGCTGAATGATGTATATATGTGGGTTCAAA
SEQ ID NO: 7	(51)	CTTAAATAACCGTATTAAAATGCTGAATGATGTATATATGTGGGTTCAAA
Consensus	(51)	CTTAAATAACCGTATTAAAATGCTGAATGATGTATATATGTGGGTTCAAA
		100
SEQ ID NO: 9	(98)	TTACATAATTGTAAGTATGTTACACATTGTATAAATATGTTTAGAGAA
SEQ ID NO: 8	(101)	TTACATAATTGTAAGTATGTTACACATTGTATAAATATGTTTAGAGAA
SEQ ID NO: 7	(101)	TTACATAATTGTAAGTATGTTACACATTGTATAAATATGTTTAGAGAA
Consensus	(101)	TTACATAATTGTAAGTATGTTACACATTGTATAAATATGTTTAGAGAA
		150
SEQ ID NO: 9	(148)	AAATGTAAACTTATATGTCTAAAGTTATAAAAGAAACATGTCCAACACAT
SEQ ID NO: 8	(151)	AAATGTAAACTTATATGTCTAAAGTTATAAAAGAAACATGTCCAACACAT
SEQ ID NO: 7	(151)	AAATGTAAACTTATATGTCTAAAGTTATAAAAGAAACATGTCCAACACAT
Consensus	(151)	AAATGTAAACTTATATGTCTAAAGTTATAAAAGAAACATGTCCAACACAT
		200
SEQ ID NO: 9	(198)	TTCAGTTAACGATTTAAATAGTATAAATTAAAAATTATCGATGATGACAAA
SEQ ID NO: 8	(201)	TTCAGTTAACGATTTAAATAGTATAAATTAAAAATTATCGATGATGACAAA
SEQ ID NO: 7	(201)	TTCAGTTAACGATTTAAATAGTATAA-TTAAAAATTATCGATGATGACAAA
Consensus	(201)	TTCAGTTAACGATTTAAATAGTATAAATTAAAAATTATCGATGATGACAAA
		250
SEQ ID NO: 9	(248)	AAATTGTAAATATAATTCACTTTAAAAAAAGTTAACGAAATTGAAAAAGGA
SEQ ID NO: 8	(251)	AAATTGTAAATATAATTCACTTTAAAAAAAGTTAACGAAATTGAAAAAGGA
SEQ ID NO: 7	(250)	AAATTGTAAATATAATTCACTTTAAAAAAAGTTAACGAAATTGAAAAAGGA
Consensus	(251)	AAATTGTAAATATAATTCACTTTAAAAAAAGTTAACGAAATTGAAAAAGGA
		300
SEQ ID NO: 9	(298)	AATATCGAGAAAAAAATATGTCGATTATATATATGTGTGAGCTGAGTGAA
SEQ ID NO: 8	(301)	AATATCGAGAAAAAAATATGTCGATTATATATATGTGTGAGCTGAGTGAA
SEQ ID NO: 7	(300)	AATATCGAGAAAAAAATATGTCGATTATATATATGTGTGAGCTGAGTGAA
Consensus	(301)	AATATCGAGAAAAAAATATGTCGATTATATATGTGTGAGCTGAGTGAA
		350
SEQ ID NO: 9	(348)	TATATATGTATATTTATTTGACTGAATATATGTGTGTATAGACAATA
SEQ ID NO: 8	(351)	TATATATGTATATTTATTTGACTGAATATATGTGTGTATAGACAATA
SEQ ID NO: 7	(350)	TATATATGTATATTTATTTGACTGAATATATGTGTGTATAGACAATA
Consensus	(351)	TATATATGTATATTTATTTGACTGAATATATGTGTGTATAGACAATA
		400
SEQ ID NO: 9	(398)	ATGCGCAGAACGCCGATCGATGAATTGTTACTGCATTTCAAATATGTG
SEQ ID NO: 8	(401)	ATGCGCAGAACGCCGATCGATGAATTGTTACTGCATTTCAAATATGTG
SEQ ID NO: 7	(400)	ATGCGCAGAACGCCGATCGATGAATTGTTACTGCATTTCAAATATGTG
Consensus	(401)	ATGCGCAGAACGCCGATCGATGAATTGTTACTGCATTTCAAATATGTG
		450
SEQ ID NO: 9	(448)	TGCATAAGCGTCCACATGTCAACCATGTTGAATTAGTTCTTCCCTGG
SEQ ID NO: 8	(451)	TGCATAAGCGTCCACATGTCAACCATGTTGAATTAGTTCTTCCCTGG
SEQ ID NO: 7	(450)	TGCATAAGCGTCCACATGTCAACCATGTTGAATTAGTTCTTCCCTGG
Consensus	(451)	TGCATAAGCGTCCACATGTCAACCATGTTGAATTAGTTCTTCCCTGG
		500
SEQ ID NO: 9	(448)	TGCATAAGCGTCCACATGTCAACCATGTTGAATTAGTTCTTCCCTGG
SEQ ID NO: 8	(451)	TGCATAAGCGTCCACATGTCAACCATGTTGAATTAGTTCTTCCCTGG
SEQ ID NO: 7	(450)	TGCATAAGCGTCCACATGTCAACCATGTTGAATTAGTTCTTCCCTGG
Consensus	(451)	TGCATAAGCGTCCACATGTCAACCATGTTGAATTAGTTCTTCCCTGG
		550

Fig. 8a

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SEQ ID NO: 9 (498)	ATGAATTACTAAGAACAGATTGATTGATAGTACTATATTAAATTATGTA	
SEQ ID NO: 8 (501)	ATGAATTACTAAGAACAGATTGATTGATAGTACTATATTAAATTATGTA	
SEQ ID NO: 7 (500)	ATGAATTACTAAGAACAGATTGATTGATAGTACTATATTAAATTATGTA	
Consensus (501)	ATGAATTACTAAGAACAGATTGATTGATAGTACTATATTAAATTATGTA	600
	551	600
SEQ ID NO: 9 (548)	GCTTTACATGTCAGGAAAATGTAGTTGCAGTATTATGTAATGTAATTAAT	
SEQ ID NO: 8 (551)	GCTTTACATGTCAGGAAAATGTAGTTGCAGTATTATGTAATGTAATTAAT	
SEQ ID NO: 7 (550)	GCTTTACATGTCAGGAAAATGTAGTTGCAGTATTATGTAATGTAATTAAT	
Consensus (551)	GCTTTACATGTCAGGAAAATGTAGTTGCAGTATTATGTAATGTAATTAAT	650
	601	650
SEQ ID NO: 9 (598)	AGGAAGTCACAGACAATTGAAAGACAATTCTTAGCTTACCTATCTCAT	
SEQ ID NO: 8 (601)	AGGAAGTCACAGACAATTGAAAGACAATTCTTAGCTTACCTATCTCAT	
SEQ ID NO: 7 (600)	AGGAAGTCACAGACAATTGAAAGACAATTCTTAGCTTACCTATCTCAT	
Consensus (601)	AGGAAGTCACAGACAATTGAAAGACAATTCTTAGCTTACCTATCTCAT	700
	651	700
SEQ ID NO: 9 (648)	GCCACACAATTATGTACTTACGACAGTAAAATGTTAAAAGCAAAA-----	
SEQ ID NO: 8 (651)	GCCACACAATTATGTACTTACGACAGTAAAATGTTAAAAGCAAAA-----	
SEQ ID NO: 7 (650)	GCCACACAATTATGTACTTACGACAGTAAAATGTTAAAAGCAAAAAGCAAAA	
Consensus (651)	GCCACACAATTATGTACTTACGACAGTAAAATGTTAAAAGCAAAA	750
	701	750
SEQ ID NO: 9 (692)	AAAAGAAAGAAGAAGAAGAAGTAATAATGGAATTATATAGAATGTACTC	
SEQ ID NO: 8 (695)	AAAAGAAAGAAGAAGAAGAAGTAATAATGGAATTATATAGAATGTACTC	
SEQ ID NO: 7 (700)	AAAAGAAAGAAGAAGAAGAAGTAATAATGGAATTATATAGAATGTACTC	
Consensus (701)	AAAAGAAAGAAGAAGAAGTAATAATGGAATTATATAGAATGTACTC	800
	751	800
SEQ ID NO: 9 (742)	TTTGTCTTCATCTGCCCTATAATTCTGCAGCAGCCAAAGCATAATAGCA	
SEQ ID NO: 8 (745)	TTTGTCTTCATCTGCCCTATAATTCTGCAGCAGCCAAAGCATAATAGCA	
SEQ ID NO: 7 (750)	TTTGTCTTCATCTGCCCTATAATTCTGCAGCAGCCAAAGCATAATAGCA	
Consensus (751)	TTTGTCTTCATCTGCCCTATAATTCTGCAGCAGCCAAAGCATAATAGCA	850
	801	850
SEQ ID NO: 9 (792)	TGCAATATGCACATATCGTTTAGGCTTTAGCCTCCACGATCTGTAA	
SEQ ID NO: 8 (795)	TGCAATATGCACATATCGTTTAGGCTTTAGCCTCCACGATCTGTAA	
SEQ ID NO: 7 (800)	TGCAATATGCACATATCGTTTAGGCTTTAGC-TCCACGATCTGTAA	
Consensus (801)	TGCAATATGCACATATCGTTTAGGCTTTAGCCTCCACGATCTGTAA	900
	851	900
SEQ ID NO: 9 (842)	TGGAAAGTAAAAAGTAAGAGATATGAAGTTCATTATGGCAGCCATGGTCC	
SEQ ID NO: 8 (845)	TGGAAAGTAAAAAGTAAGAGATATGAAGTTCATTATGGCAGCCATGGTCC	
SEQ ID NO: 7 (849)	TGGAAAGTAAAAAGTAAGAGATATGAAGTTCATTATGGCAGCCATGGTCC	
Consensus (851)	TGGAAAGTAAAAAGTAAGAGATATGAAGTTCATTATGGCAGCCATGGTCC	950
	901	950
SEQ ID NO: 9 (892)	CAGGGAAGCACTAGAAGATATGAAATGACATAAAAGGTACCACATGCATAA	
SEQ ID NO: 8 (895)	CAGGGAAGCACTAGAAGATATGAAATGACATAAAAGGTACCACATGCATAA	
SEQ ID NO: 7 (899)	CAGGGAAGCACTAGAAGATATGAAATGAC-TAAAAGGTACCACATGCATAA	
Consensus (901)	CAGGGAAGCACTAGAAGATATGAAATGACATAAAAGGTACCACATGCATAA	1000
	951	1000
SEQ ID NO: 9 (942)	TGCTTTAAATGCTTGCTATAGAATCAAAAATGAAGAGATGTGACAAATT	
SEQ ID NO: 8 (945)	TGCTTTAAATGCTTGCTATAGAATCAAAAATGAAGAGATGTGACAAATT	
SEQ ID NO: 7 (948)	TGCTTTAAATGCTTGCTATAGAATCAAAAATGAAGAGATGTGACAAATT	
Consensus (951)	TGCTTTAAATGCTTGCTATAGAATCAAAAATGAAGAGATGTGACAAATT	

Fig. 8b

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	1001	1050
SEQ ID NO: 9 (992)	GTTACATCTAATACGCAATAATTGACAAAGACGACTATGC GTT TATATA	
SEQ ID NO: 8 (995)	GTTACATCTAATACGCAATAATTGACAAAGACGACTATGC GTT TATATA	
SEQ ID NO: 7 (998)	GTTACATCTAATACGCAATAATTGACAAAGACGACTATGC GTT TATATA	
Consensus (1001)	GTTACATCTAATACGCAATAATTGACAAAGACGACTATGC GTT TATATA	
	1051	1100
SEQ ID NO: 9 (1042)	TTTATTTAATTAGTTGGCGTCTCTTATTATAAAGAAAATAAGGGCAGTG	
SEQ ID NO: 8 (1045)	TTTATTTAATTAGTTGGCGTCTCTTATTATAAAGAAAATAAGGGCAGTG	
SEQ ID NO: 7 (1048)	TTTATTTAATTAGTTGGCGTCTCTTATTATAAAGAAAATAAGGGCAGTG	
Consensus (1051)	TTTATTTAATTAGTTGGCGTCTCTTATTATAAAGAAAATAAGGGCAGTG	
	1101	1150
SEQ ID NO: 9 (1092)	TCAACATTC CAGGCAACTAGTTAGTTATTTATTTCTTGT TATAATT	
SEQ ID NO: 8 (1095)	TCAACATTC CAGGCAACTAGTTAGTTATTTATTTCTTGT TATAATT	
SEQ ID NO: 7 (1098)	TCAACATTC CAGGCAACTAGTTAGTTATTTATTTCTTGT TATAATT	
Consensus (1101)	TCAACATTC CAGGCAACTAGTTAGTTATTTATTTCTTGT TATAATT	
	1151	1200
SEQ ID NO: 9 (1142)	ATTCCATATAGCTAGCTGTCTCTATCTAACCTAAATCCGTTTCCACAA	
SEQ ID NO: 8 (1145)	ATTCCATATAGCTAGCTGTCTCTATCTAACCTAAATCCGTTTCCACAA	
SEQ ID NO: 7 (1148)	ATTCCATATAGCTAGCTGTCTCTATCTAACCTAAATCCGTTTCCACAA	
Consensus (1151)	ATTCCATATAGCTAGCTGTCTCTATCTAACCTAAATCCGTTTCCACAA	
	1201	1250
SEQ ID NO: 9 (1192)	CCAAC TTGGTCGCATTGGTCAAAAAACTCAATATCAATATTTCGAAAT	
SEQ ID NO: 8 (1195)	CCAAC TTGGTCGCATTGGTCAAAAAACTCAATATCAATATTTCGAAAT	
SEQ ID NO: 7 (1198)	CCAAC TTGGT-----CCA AAA ACTCAATATCAATATTTCAAAT	
Consensus (1201)	CCAAC TTGGTCGCATTGGTCAAAAAACTCAATATCAATATTTCGAAAT	
	1251	1300
SEQ ID NO: 9 (1242)	AGTTTAGCATTGTTAGGAAGAGAATTGTAAGAGATAAAATCTAAGTAC	
SEQ ID NO: 8 (1245)	AGTTTAGCATTGTTAGGAAGAGAATTGTAAGAGATAAAATCTAAGTAC	
SEQ ID NO: 7 (1239)	AGTTTAGCATTGTTAGGAAGAGAATTGTAAGAGATAAAATCTAAGTAC	
Consensus (1251)	AGTTTAGCATTGTTAGGAAGAGAATTGTAAGAGATAAAATCTAAGTAC	
	1301	1350
SEQ ID NO: 9 (1292)	TCCACCTACCAAGATAAAATAGTTGGATAATGGTAAAAAGTTGTAT	
SEQ ID NO: 8 (1295)	TCCACCTACCAAGATAAAATAGTTGGATAATGGTAAAAAGTTGTAT	
SEQ ID NO: 7 (1289)	TCCACCTACCAAGATAAAATAGTTGGATAATGGTAAAAA-GTTGTAT	
Consensus (1301)	TCCACCTACCAAGATAAAATAGTTGGATAATGGTAAAAAGTTGTAT	
	1351	1393
SEQ ID NO: 9 (1342)	AAAGGGCAACACTACCTCTCCTAATGGCAGTA-----	
SEQ ID NO: 8 (1345)	AAAGGGCAACACTACCTCTCCTAATGGCAGTACCAAAACCC AAG	
SEQ ID NO: 7 (1338)	AAAGGGCAACACTACCTCTCCTAATGGCAGTACCAAAACCC AAG	
Consensus (1351)	AAAGGGCAACACTACCTCTCCTAATGGCAGTACCAAAACCC AAG	

Fig. 8c

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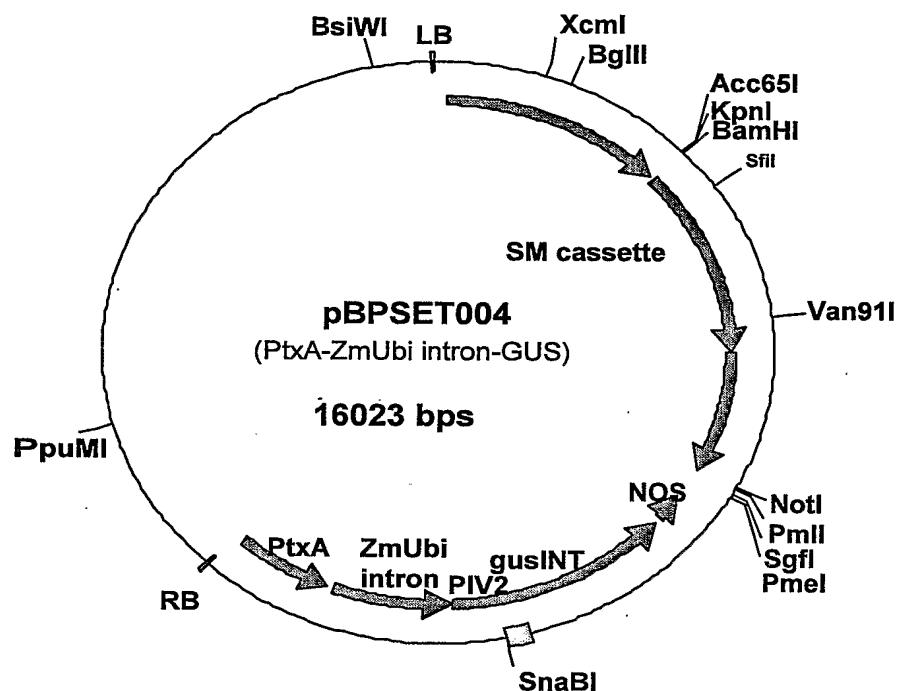


Fig. 9